

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 35, line 28, as follows:

Bioinformatics analyses. Bioinformatics analysis was performed with the NCBI Human Genome databases (available on the Web at ncbi.nlm.nih.gov/genome/guide/human) and the Celera Discovery System ([available online at cds.celera.com/cdshttp://eds.celera.com/eds](http://cds.celera.com/cdshttp://eds.celera.com/eds)). Gene finding was performed with BLASTX (available on the Web at ncbi.nlm.nih.gov/BLAST) and GENESCAN and FGENES software (GeneMachine, DIR, NIH, [available online at genome.nhgri.nih.gov/genemachine/](http://genome.nhgri.nih.gov/genemachine/)http://genome.nhgri.nih.gov/genemachine/). SNPs were developed using the SNP database ([available on the Web at ncbi.nlm.nih.gov/SNP/](http://ncbi.nlm.nih.gov/SNP/))[\(available on the Web at ncbi.nlm.nih.gov/SNP/\)](http://http://ncbi.nlm.nih.gov/SNP/).